WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule that comprises a polynucleotide sequence that encodes an α2,3-sialyltransferase polypeptide having an amino acid sequence at least about 75% identical to an amino acid sequence as set forth in SEQ. ID. NO: 2 over a region at least about 50 amino acids in length when compared using the BLASTP algorithm with a wordlength (W) of 3, and the BLOSUM62 scoring matrix.

2. The nucleic acid of claim 1, wherein the polynucleotide sequence encodes an α2,3-sialyltransferase having an amino acid sequence as shown in SEQ. ID. NO:2.

3. The nucleic acid of claim 1, wherein the polynucleotide sequence encodes a α2,3-sialyltransferase polypeptide having at least about 328 amino acids.

4. The nucleic acid of claim 3, wherein the polynucleotide sequence encodes a α2,3-sialyltransferase polypeptide having about 430 amino acids.

5. The nucleic acid of claim 1, wherein the polynucleotide sequence is at least about 75% identical to a nucleic acid sequence as set forth in SEQ. ID. NO:1 over a region at least about 120 nucleotides in length when compared using the BLASTN algorithm with a wordlength (W) of 11, M=5, and N= -4.

6. The nucleic acid of claim 1, wherein the polynucleotide sequence hybridizes to a nucleic acid having a sequence as shown in SEQ. ID. NO:1 under stringent conditions.

7. The nucleic acid of claim 1, wherein the polynucleotide sequence is as shown in SEQ. ID. NO:1.

8. The nucleic acid of claim 1, wherein the polynucleotide sequence is derived from a *Campylobacter* species.

9. The nucleic acid of claim 8, wherein the *Campylobacter* species is *C. jejuni*.

10. The nucleic acid of claim 9, wherein the *C. jejuni* is strain OH4384.

11. The nucleic acid of claim 1, wherein the polynucleotide sequence is operably linked to a second polynucleotide sequence that encodes a second polypeptide.

12. The nucleic acid of claim 11, wherein the second polypeptide comprises a tag suitable for affinity purification of a fusion protein produced by expression of the nucleic acid.

13. The nucleic acid of claim 1, further comprising a promoter sequence operably linked to the polynucleotide sequence.

14. The nucleic acid of claim 13, wherein the promoter is active in eukaryotic cells.

15. The nucleic acid of claim 13, wherein the promoter is active in prokaryotic cells.

16. The nucleic acid of claim 15, wherein the promoter is active in *E. coli.*

17. An isolated nucleic acid molecule which encodes an α2,3-sialyltransferase polypeptide having an amino acid sequence as shown in SEQ. ID. No. 2.

18. A cell comprising a recombinant expression cassette containing a promoter operably linked to a polynucleotide sequence which encodes an α2,3-sialyltransferase polypeptide and which is least about 75% identical to a polynucleotide sequence as set forth in SEQ. ID. NO:1 over a region at least about 120 nucleotides in length when compared using the BLASTN algorithm with a wordlength (W) of 11, M=5, and N= -4.

19. The cell of claim 18, wherein the polynucleotide hybridizes to a nucleic acid having a sequence as shown in SEQ. ID. No. 1 under stringent conditions.

20. The cell of claim 18, wherein the cell is a prokaryotic cell.

21. The cell of claim 20, wherein the cell is *E. coli*.

22. The cell of claim 18, wherein the cell is a eukaryotic cell.

23. The cell of claim 18, wherein the polynucleotide sequence is as shown in SEQ. ID. No. 1.

24. An isolated α2,3-sialyltransferase polypeptide having an amino acid sequence at least about 75% identical to an amino acid sequence as set forth in SEQ. ID. NO: 2 over a region at least about 50 amino acids in length when compared using the BLASTP algorithm with a wordlength (W) of 3, and the BLOSUM62 scoring matrix.

25. The α2,3-sialyltransferase polypeptide of claim 24 which has at least about 328 amino acids.

26. The α2,3-sialyltransferase polypeptide of claim 24 which has about 430 amino acids.

27. The α2,3-sialyltransferase polypeptide of claim 24 which has a sequence as shown in SEQ. ID. NO.: 2.

28. A method of adding a sialic acid residue to an acceptor molecule comprising a terminal galactose residue, the method comprising contacting the acceptor molecule with an activated sialic acid molecule and an α2,3-sialyltransferase having an amino acid sequence at least about 75% identical over a region at least about 50 amino acids in length when compared to the amino acid sequence shown in SEQ. ID. No. 2 using the BLASTP algorithm with a wordlength (W) of 3, and the BLOSUM62 scoring matrix.

29. The method of claim 28, wherein the terminal galactose residue is linked through a β linkage to a second residue in the acceptor molecule.

30. The method of claim 29, wherein the linkage is a β1,4 linkage.

31. The method of claim 30, wherein the second residue is a Glc or a GlcNAc.

32. The method of claim 29, wherein the linkage is a β1,3 linkage.

33. The method of claim 32, wherein the second residue is a GlcNAc or a GalNAc.

34. The method of claim 28, wherein the activated sialic acid is CMP-Neu5Ac.